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TECH CENTER 1600/2900

Tue Jun 19 15:59:27 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpanda/templ/ss.DNA35639 (1813 bp)

Sequences producing High-scoring Segment Pairs:				Frame	Score	Match	Pct	E-val
1	P_AAC97441	Human angiogenesis-associated protein PR		+	1813	1813	100	0.0
2	P_AAF72379	Human PRO246 cDNA.		+	1813	1813	100	0.0
3	P_AAC87040	Nucleotide sequence of human polypeptide		+	1813	1813	100	0.0
4	P_AAF60372	PRO246 coding sequence.		+	1813	1813	100	0.0
5	P_AAA30052	Human PRO246 nucleotide sequence.		+	1813	1813	100	0.0
6	P_AAX28436	EGF-like homologue PRO246 coding sequenc		+	1813	1813	100	0.0
7	P_AAX52221	Protein PRO246 cDNA clone DNA35639-1172.		+	1813	1813	100	0.0
8	AX076924	Sequence 36 from Patent WO0105836.		+	1813	1813	100	0.0
9	P_AAF93785	Human cDNA encoding a membrane or secret		+	1809	1809	100	0.0
10	AX136161	Sequence 83 from Patent EP1067182.		+	1809	1809	100	0.0
11	P_AAA23441	cDNA encoding human secreted protein vc5		+	1806	1813	100	0.0
12	AF361746	Homo sapiens endothelial cell-selective		+	1805	1811	100	0.0
13	P_AAH02949	Human shear stress-response coding seque		+	1801	1807	100	0.0
14	P_AAZ65278	Human secreted protein gene 29.		+	1785	1804	100	0.0
15	P_AAF45017	Human secreted protein related coding se		+	1731	1795	99	0.0
16	P_AAF45016	Human secreted protein related coding se		+	1731	1795	99	0.0
17	P_AAF45014	Human secreted protein related coding se		+	1731	1795	99	0.0

>1 P_AAC97441 Human angiogenesis-associated protein PRO246 cDNA, SEQ ID NO:95.
(1813 bp) [1 seg]

Score = 1813 (3594 bits), Expect = 0.0

Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+

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DNA35639      1  GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
*****
P_AAC97441    1  GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

DNA35639     61  CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
*****
P_AAC97441    61  CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

DNA35639    121  GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
*****
P_AAC97441   121  GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

DNA35639    181  GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
*****
P_AAC97441   181  GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC

DNA35639    241  GGTTCGAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGG
*****
P_AAC97441   241  GGTTCGAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGG

DNA35639    301  AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
*****
P_AAC97441   301  AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

DNA35639    361  AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
*****
P_AAC97441   361  AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
```

BLAST RESULTS A-1

DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
P_AAC97441	421	CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
P_AAC97441	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC
P_AAC97441	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
P_AAC97441	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
P_AAC97441	661	GTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCTGCTTCCATGG
P_AAC97441	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCTGCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
P_AAC97441	781	CTGGAGTCTATGTCTGCAAGGCCACCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
P_AAC97441	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
P_AAC97441	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
P_AAC97441	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC
P_AAC97441	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC
DNA35639	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
P_AAC97441	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCACCCCTCAACCAATAT
P_AAC97441	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCACCCCTCAACCAATAT
DNA35639	1201	CCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
P_AAC97441	1201	CCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639	1261	TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTGGCTA

BLAST RESULTS A-2

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*****
P_AAC97441 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA
DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
*****
P_AAC97441 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
*****
P_AAC97441 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
*****
P_AAC97441 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAC97441 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
*****
P_AAC97441 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
P_AAC97441 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
P_AAC97441 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
*****
P_AAC97441 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
DNA35639 1801 TTTGTATGAAAAA
*****
P_AAC97441 1801 TTTGTATGAAAAA

```

>2 P_AAF72379 Human PRO246 cDNA. (1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/-

```

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGCGCGTCGCGCAGCCT
*****
P_AAF72379 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGCGCGTCGCGCAGCCT
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
*****
P_AAF72379 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
*****
P_AAF72379 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
*****

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BLAST RESULTS A-3

P_AAF72379	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGGCCAGCTGCAACTGCACTTGCCCCGCAACC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGG *****
P_AAF72379	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG *****
P_AAF72379	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT *****
P_AAF72379	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA *****
P_AAF72379	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
P_AAF72379	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC *****
P_AAF72379	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA *****
P_AAF72379	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCGCTGTCCAATACCAAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG *****
P_AAF72379	661	GTAAGCCCGCTGTCCAATACCAAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG *****
P_AAF72379	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC *****
P_AAF72379	781	CTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGG *****
P_AAF72379	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGG
DNA35639	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG *****
P_AAF72379	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA *****
P_AAF72379	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC *****
P_AAF72379	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC

BLAST RESULTS A-4

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DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
*****
P_AAF72379 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT
*****
P_AAF72379 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT

DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****
P_AAF72379 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTTGGCTA
*****
P_AAF72379 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTTGGCTA

DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACTCTAGCACAGAGGCCTGAGTCATG
*****
P_AAF72379 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACTCTAGCACAGAGGCCTGAGTCATG

DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
*****
P_AAF72379 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA

DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGATCTGGA
*****
P_AAF72379 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGATCTGGA

DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAF72379 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
*****
P_AAF72379 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA

DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
P_AAF72379 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGTATTGAT

DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
P_AAF72379 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
*****
P_AAF72379 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG

DNA35639 1801 TTTGTATGAAAAA
*****
P_AAF72379 1801 TTTGTATGAAAAA

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>3 P_AAC87040 Nucleotide sequence of human polypeptide PRO246. (1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/-

```

BLAST RESULTS A-5

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
P_AAC87040	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
P_AAC87040	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639	121	GGGCCATGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
P_AAC87040	121	GGGCCATGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
P_AAC87040	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGG
P_AAC87040	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
P_AAC87040	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
P_AAC87040	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
P_AAC87040	421	CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
P_AAC87040	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCC
P_AAC87040	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
P_AAC87040	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
P_AAC87040	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
P_AAC87040	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
P_AAC87040	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG

BLAST RESULTS A-U

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*****
P_AAC87040 841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
*****
P_AAC87040 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
*****
P_AAC87040 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC
*****
P_AAC87040 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC
DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA
*****
P_AAC87040 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA
DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCTCAACCAATAT
*****
P_AAC87040 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCTCAACCAATAT
DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****
P_AAC87040 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
*****
P_AAC87040 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
*****
P_AAC87040 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
*****
P_AAC87040 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
*****
P_AAC87040 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAC87040 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639 1561 CTA CTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCTTGA
*****
P_AAC87040 1561 CTA CTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCTTGA
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
P_AAC87040 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGTTTTACTGGGGCAGAGGATAGGAATCTCTTAT
*****

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BLAST RESULTS A-7

P_AAC87040 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTGCAAATTTAAATAAAGATACATAATG

P_AAC87040 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTGCAAATTTAAATAAAGATACATAATG

DNA35639 1801 TTTGTATGAAAAA

P_AAC87040 1801 TTTGTATGAAAAA

>4 P_AAF60372 PRO246 coding sequence. (1813 bp) [1 seg]
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DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

P_AAF60372 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

P_AAF60372 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

P_AAF60372 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC

P_AAF60372 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC

DNA35639 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGG

P_AAF60372 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGG

DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

P_AAF60372 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

DNA35639 361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

P_AAF60372 361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

P_AAF60372 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

DNA35639 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG

P_AAF60372 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG

DNA35639 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC

P_AAF60372 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC

DNA35639 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA

P_AAF60372 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA

BLAST RESULTS A-B

DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
P_AAF60372	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
P_AAF60372	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCACTGCCAATGTAATGTGACGC
P_AAF60372	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCACTGCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
P_AAF60372	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
P_AAF60372	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCTGCCCTGGCCCA
P_AAF60372	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
P_AAF60372	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
DNA35639	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
P_AAF60372	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCACCCCTCAACCAATAT
P_AAF60372	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCACCCCTCAACCAATAT
DNA35639	1201	CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
P_AAF60372	1201	CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639	1261	TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTGGCTA
P_AAF60372	1261	TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTGGCTA
DNA35639	1321	AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
P_AAF60372	1321	AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
P_AAF60372	1381	GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
P_AAF60372	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

BLAST RESULTS A-9

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DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAF60372 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGA
*****
P_AAF60372 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGA

DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
P_AAF60372 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
P_AAF60372 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

DNA35639 1741 TAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
*****
P_AAF60372 1741 TAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG

DNA35639 1801 TTTGTATGAAAAA
*****
P_AAF60372 1801 TTTGTATGAAAAA

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>5 P_AAA30052 Human PRO246 nucleotide sequence. (1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/-

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DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
*****
P_AAA30052 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
*****
P_AAA30052 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
*****
P_AAA30052 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC
*****
P_AAA30052 181 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC

DNA35639 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGG
*****
P_AAA30052 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGG

DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
*****
P_AAA30052 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

DNA35639 361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
*****
P_AAA30052 361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

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BLAST RESULTS A-10

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*****
P_AAA30052 421 CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639 481 AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
*****
P_AAA30052 481 AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC
*****
P_AAA30052 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC
DNA35639 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
*****
P_AAA30052 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639 661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
*****
P_AAA30052 661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
*****
P_AAA30052 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639 781 CTGGAGTCTATGTCTGCAAGGCCCAACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
*****
P_AAA30052 781 CTGGAGTCTATGTCTGCAAGGCCCAACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639 841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
*****
P_AAA30052 841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
*****
P_AAA30052 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
*****
P_AAA30052 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
*****
P_AAA30052 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
*****
P_AAA30052 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTCAACCAATAT
*****
P_AAA30052 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTCAACCAATAT
DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****
P_AAA30052 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
*****

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BLAST RESULTS A-11

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P_AAA30052 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA
DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
*****
P_AAA30052 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
*****
P_AAA30052 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
*****
P_AAA30052 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAA30052 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639 1561 CTA CTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
*****
P_AAA30052 1561 CTA CTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
P_AAA30052 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
P_AAA30052 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
DNA35639 1741 TAAACTAACATGAAATATGTGTTGTTTTATTGCAAATTTAAATAAAGATACATAATG
*****
P_AAA30052 1741 TAAACTAACATGAAATATGTGTTGTTTTATTGCAAATTTAAATAAAGATACATAATG
DNA35639 1801 TTTGTATGAAAAA
*****
P_AAA30052 1801 TTTGTATGAAAAA

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>6 P_AAX28436 EGF-like homologue PRO246 coding sequence. DNA, PAT 22-JUN-1999 (1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+

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DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
*****
P_AAX28436 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGA
*****
P_AAX28436 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
*****
P_AAX28436 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
*****

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BLAST RESULTS A-12

P_AAX28436	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGG *****
P_AAX28436	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG *****
P_AAX28436	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT *****
P_AAX28436	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA *****
P_AAX28436	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
P_AAX28436	481	AAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC *****
P_AAX28436	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA *****
P_AAX28436	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG *****
P_AAX28436	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG *****
P_AAX28436	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC *****
P_AAX28436	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGTTGCTGGAGCTGTTGTGGGTACCCTGG *****
P_AAX28436	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG *****
P_AAX28436	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA *****
P_AAX28436	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC *****
P_AAX28436	1021	AGAGCTCAGACACAATCTCCAAGAAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC

BLAST RESULTS A-12

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DNA35639 1081 TCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
*****
P_AAX28436 1081 TCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT
*****
P_AAX28436 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT

DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****
P_AAX28436 1201 CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA
*****
P_AAX28436 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA

DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
*****
P_AAX28436 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG

DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
*****
P_AAX28436 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA

DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
*****
P_AAX28436 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAX28436 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
*****
P_AAX28436 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA

DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
P_AAX28436 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
P_AAX28436 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
*****
P_AAX28436 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG

DNA35639 1801 TTTGTATGAAAAA
*****
P_AAX28436 1801 TTTGTATGAAAAA

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BLAST RESULTS A-A

>7 P_AAX52221 Protein PRO246 cDNA clone DNA35639-1172. DNA, PAT 25-JUN-1999
(1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/-

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
P_AAX52221	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
P_AAX52221	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639	121	GGGCCATGATTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
P_AAX52221	121	GGGCCATGATTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
P_AAX52221	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG
P_AAX52221	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
P_AAX52221	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
P_AAX52221	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
P_AAX52221	421	CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
P_AAX52221	481	AAGACTCTGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTTCCTCCAGCTCCTCCATCCTGCC
P_AAX52221	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTTCCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
P_AAX52221	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
P_AAX52221	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
P_AAX52221	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
P_AAX52221	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC

BLAST RESULTS A-15

DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG

P_AAX52221	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639	901	TTGGAAGTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG

P_AAX52221	901	TTGGAAGTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA

P_AAX52221	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC

P_AAX52221	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCCC
DNA35639	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

P_AAX52221	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCTCAACCAATAT

P_AAX52221	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCTCAACCAATAT
DNA35639	1201	CCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

P_AAX52221	1201	CCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639	1261	TGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTGGCTA

P_AAX52221	1261	TGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTGGCTA
DNA35639	1321	AAGGATTTGGGGTCTCTCCTTCTTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG

P_AAX52221	1321	AAGGATTTGGGGTCTCTCCTTCTTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA

P_AAX52221	1381	GGAAAGAGTCACACTCCTGACCCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

P_AAX52221	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639	1501	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

P_AAX52221	1501	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639	1561	CTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGA

P_AAX52221	1561	CTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGA
DNA35639	1621	TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

P_AAX52221	1621	TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639	1681	ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

BLAST RESULTS A-110

P_AAX52221 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG

P_AAX52221 1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
DNA35639 1801 TTTGTATGAAAAA

P_AAX52221 1801 TTTGTATGAAAAA

>8 AX076924 Sequence 36 from Patent WO0105836. (1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/-

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

AX076924 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

AX076924 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

AX076924 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCATTGCCCGCCAACC

AX076924 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCATTGCCCGCCAACC
DNA35639 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGGG

AX076924 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGGG
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

AX076924 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639 361 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

AX076924 361 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

AX076924 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG

AX076924 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC

AX076924 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC
DNA35639 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA

BLAST RESULTS A-17

AX076924 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA

DNA35639 661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG

AX076924 661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG

DNA35639 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG

AX076924 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG

DNA35639 781 CTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC

AX076924 781 CTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC

DNA35639 841 TGGAAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG

AX076924 841 TGGAAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG

DNA35639 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG

AX076924 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG

DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA

AX076924 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA

DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC

AX076924 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC

DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

AX076924 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT

AX076924 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT

DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

AX076924 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA

AX076924 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA

DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG

AX076924 1321 AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG

DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGA^{AA}

AX076924 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGA^{AA}

DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

AX076924 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

BLAST RESULTS A-18

DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

 AX076924 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

 DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA

 AX076924 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA

 DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

 AX076924 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

 DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

 AX076924 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

 DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAATG

 AX076924 1741 TAAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAATG

 DNA35639 1801 TTTGTATGAAAAA

 AX076924 1801 TTTGTATGAAAAA

>9 P_AAF93785 Human cDNA encoding a membrane or secretory protein clone
 PSEC0086. (1821 bp) [1 seg]
 Score = 1809 (3586 bits), Expect = 0.0
 Identities = 1809/1809 (100%), at 1,12-1809,1820, Strand +/-

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

 P_AAF93785 12 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

 DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGA

 P_AAF93785 72 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGA

 DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

 P_AAF93785 132 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

 DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCAACC

 P_AAF93785 192 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCAACC

 DNA35639 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG

 P_AAF93785 252 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG

 DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

 P_AAF93785 312 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

 DNA35639 361 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

 P_AAF93785 372 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

BLAST RESULTS A-19

DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

P_AAF93785	432	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG

P_AAF93785	492	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC

P_AAF93785	552	GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA

P_AAF93785	612	GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG

P_AAF93785	672	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG

P_AAF93785	732	CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC

P_AAF93785	792	CTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGG

P_AAF93785	852	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGG
DNA35639	901	TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG

P_AAF93785	912	TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCCTGCCCTGGCCCA

P_AAF93785	972	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC

P_AAF93785	1032	AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
DNA35639	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

P_AAF93785	1092	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT

P_AAF93785	1152	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT
DNA35639	1201	CCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

P_AAF93785	1212	CCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

BLAST RESULTS A-20

BLAST RESULTS A-21

DNA35639	1261	TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA

P_AAF93785	1272	TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
DNA35639	1321	AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG

P_AAF93785	1332	AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA

P_AAF93785	1392	GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

P_AAF93785	1452	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639	1501	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

P_AAF93785	1512	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639	1561	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA

P_AAF93785	1572	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
DNA35639	1621	TCTGTACCCCACTTATCTAACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

P_AAF93785	1632	TCTGTACCCCACTTATCTAACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639	1681	ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGAATCTCTTAT

P_AAF93785	1692	ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGAATCTCTTAT
DNA35639	1741	TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG

P_AAF93785	1752	TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
DNA35639	1801	TTTGTATGA

P_AAF93785	1812	TTTGTATGA

>10 AX136161 Sequence 83 from Patent EP1067182. (1821 bp) [1 seg]
Score = 1809 (3586 bits), Expect = 0.0
Identities = 1809/1809 (100%), at 1,12-1809,1820, Strand +/-

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

AX136161	12	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

AX136161	72	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639	121	GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

AX136161	132	GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC

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*****
AX136161 192 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639 241 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGTCTCCAGCGTGGTACACCTGCACGGGG
*****
AX136161 252 GGTTCAGGCGGTGGAGGGAGGGGAAGTGGTGTCTCCAGCGTGGTACACCTGCACGGGG
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
*****
AX136161 312 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639 361 AAAAGGAGGATCAGGTGTTGTCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
*****
AX136161 372 AAAAGGAGGATCAGGTGTTGTCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
*****
AX136161 432 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
*****
AX136161 492 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC
*****
AX136161 552 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC
DNA35639 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
*****
AX136161 612 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639 661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
*****
AX136161 672 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
*****
AX136161 732 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639 781 CTGGAGTCTATGTCTGCAAGGCCACCAATGAGGTGGGCACTGCCCCAATGTAATGTGACGC
*****
AX136161 792 CTGGAGTCTATGTCTGCAAGGCCACCAATGAGGTGGGCACTGCCCCAATGTAATGTGACGC
DNA35639 841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGG
*****
AX136161 852 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGG
DNA35639 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
*****
AX136161 912 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCTGCCCTGGCCCA
*****
AX136161 972 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCTGCCCTGGCCCA
DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC
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BLAST RESULTS A-22

BLAST RESULTS A-23

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AX136161 1032 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTGTCACCTCCGCACGAGCCC
DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA
*****
AX136161 1092 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA
DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT
*****
AX136161 1152 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAATAT
DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****
AX136161 1212 CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
*****
AX136161 1272 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
*****
AX136161 1332 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
*****
AX136161 1392 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
*****
AX136161 1452 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
AX136161 1512 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
*****
AX136161 1572 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
AX136161 1632 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
AX136161 1692 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
DNA35639 1741 TAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
*****
AX136161 1752 TAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG
DNA35639 1801 TTTGTATGA
*****
AX136161 1812 TTTGTATGA
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>11 P_AAA23441 cDNA encoding human secreted protein vc51_1, SEQ ID NO:37. (1954 bp) [1 seg]
Score = 1806 (3580 bits), Expect = 0.0

Identities = 1813/1814 (99%), Gaps = 1/1814 (0%), at 1,13-1813,1826, Strand +/+

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DNA35639      1  GGAGCCGCCCTGGGTGTCAGC-GGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCC
*****
P_AAA23441    13  GGAGCCGCCCTGGGTGTCAGCGGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCC

DNA35639      60  TCGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGG
*****
P_AAA23441    73  TCGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGG

DNA35639     120  AGGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTG
*****
P_AAA23441   133  AGGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTG

DNA35639     180  GGGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCAAC
*****
P_AAA23441   193  GGGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCAAC

DNA35639     240  CGGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGG
*****
P_AAA23441   253  CGGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGG

DNA35639     300  GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA
*****
P_AAA23441   313  GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA

DNA35639     360  GAAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA
*****
P_AAA23441   373  GAAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA

DNA35639     420  TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAG
*****
P_AAA23441   433  TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAG

DNA35639     480  AAAGACTCTGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG
*****
P_AAA23441   493  AAAGACTCTGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG

DNA35639     540  GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC
*****
P_AAA23441   553  GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC

DNA35639     600  CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG
*****
P_AAA23441   613  CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG

DNA35639     660  AGTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT
*****
P_AAA23441   673  AGTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT

DNA35639     720  GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATG
*****
P_AAA23441   733  GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATG

DNA35639     780  GCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACG
*****
P_AAA23441   793  GCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACG
```

BLAST RESULTS A-24

DNA35639	840	CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTG

P_AAA23441	853	CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTG
DNA35639	900	GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTAACACCGCCGGGGCAAGGCCCTG

P_AAA23441	913	GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTAACACCGCCGGGGCAAGGCCCTG
DNA35639	960	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC

P_AAA23441	973	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC
DNA35639	1020	AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCC

P_AAA23441	1033	AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTACCTCCGCACGAGCC
DNA35639	1080	CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCC

P_AAA23441	1093	CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCC
DNA35639	1140	AGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATA

P_AAA23441	1153	AGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATA
DNA35639	1200	TCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTG

P_AAA23441	1213	TCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTG
DNA35639	1260	ATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCT

P_AAA23441	1273	ATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCT
DNA35639	1320	AAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCAT

P_AAA23441	1333	AAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCAT
DNA35639	1380	GGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAA

P_AAA23441	1393	GGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAA
DNA35639	1440	AACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGATCTGG

P_AAA23441	1453	AACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGATCTGG
DNA35639	1500	AATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTA

P_AAA23441	1513	AATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTA
DNA35639	1560	GCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTG

P_AAA23441	1573	GCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTG
DNA35639	1620	ATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGA

P_AAA23441	1633	ATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGA

BLAST RESULTS A-25

DNA35639 1680 TATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTA

 P_AAA23441 1693 TATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTA
 DNA35639 1740 TTAAACTAACATGAAATATGTGTTGTTTTTCATTGCAAATTTAAATAAGATAACATAAT

 P_AAA23441 1753 TTAAACTAACATGAAATATGTGTTGTTTTTCATTGCAAATTTAAATAAGATAACATAAT
 DNA35639 1800 GTTTGTATGAAAAA

 P_AAA23441 1813 GTTTGTATGAAAAA

>12 AF361746 Homo sapiens endothelial cell-selective adhesion molecule (ESAM)
 (1838 bp) [1 seg]
 Score = 1805 (3578 bits), Expect = 0.0
 Identities = 1811/1813 (99%), at 1,14-1813,1826, Strand +/+

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

 AF361746 14 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
 DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGA

 AF361746 74 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGA
 DNA35639 121 GGGCCATGATTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

 AF361746 134 GGGCCATGATTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
 DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC

 AF361746 194 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
 DNA35639 241 GGTGTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGGG

 AF361746 254 GGTGTCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGGG
 DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG

 AF361746 314 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
 DNA35639 361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

 AF361746 374 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
 DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

 AF361746 434 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
 DNA35639 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG

 AF361746 494 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
 DNA35639 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCC

 AF361746 554 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCC

BLAST RESULTS A-24

DNA35639 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
 AF361746 614 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
 DNA35639 661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
 AF361746 674 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
 DNA35639 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
 AF361746 734 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
 DNA35639 781 CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
 AF361746 794 CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
 DNA35639 841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
 AF361746 854 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
 DNA35639 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
 AF361746 914 TTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
 DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCCA
 AF361746 974 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCCA
 DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
 AF361746 1034 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
 DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
 AF361746 1094 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
 DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCTCAACCAATAT
 AF361746 1154 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCTCAACCAATAT
 DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
 AF361746 1214 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
 DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTTGGCTA
 AF361746 1274 TGATGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTTGGCTA
 DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
 AF361746 1334 AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
 DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
 AF361746 1394 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
 DNA35639 1441 ACCATCTCAGTAAGACCTAAGTCTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

BLAST RESULTS A-27

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*****
AF361746 1454 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
AF361746 1514 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
*****
AF361746 1574 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
*****
AF361746 1634 TCTGTACCCACCCCTATCTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
*****
AF361746 1694 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAATG
*****
AF361746 1754 TAAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAATG
DNA35639 1801 TTTGTATGAAAAA
*****
AF361746 1814 TTTGTATGAAAAA

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BLAST RESULTS A-20

>13 P_AAH02949 Human shear stress-response coding sequence SEQ ID NO: 143. (1827 bp) [1 seg]
 Score = 1801 (3570 bits), Expect = 0.0
 Identities = 1807/1809 (99%), at 1,13-1809,1821, Strand +/-

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DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
*****
P_AAH02949 13 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGA
*****
P_AAH02949 73 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
*****
P_AAH02949 133 GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
*****
P_AAH02949 193 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG
*****
P_AAH02949 253 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
*****
P_AAH02949 313 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639 361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

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*****
P_AAH02949 373 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
*****
P_AAH02949 433 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA
DNA35639 481 AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
*****
P_AAH02949 493 AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639 541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCC
*****
P_AAH02949 553 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCC
DNA35639 601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
*****
P_AAH02949 613 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639 661 GTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
*****
P_AAH02949 673 GTAAGCCTGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG
DNA35639 721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
*****
P_AAH02949 733 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG
DNA35639 781 CTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
*****
P_AAH02949 793 CTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGC
DNA35639 841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
*****
P_AAH02949 853 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG
DNA35639 901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
*****
P_AAH02949 913 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG
DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
*****
P_AAH02949 973 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA
DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
*****
P_AAH02949 1033 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCCC
DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
**
P_AAH02949 1093 TCTGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT
*****
P_AAH02949 1153 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT
DNA35639 1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****

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BLAST RESULTS A-29

P_AA02949 1213 CCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
DNA35639 1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA

P_AA02949 1273 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGGCTA
DNA35639 1321 AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG

P_AA02949 1333 AAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA

P_AA02949 1393 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAA
DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

P_AA02949 1453 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

P_AA02949 1513 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCTTGA

P_AA02949 1573 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCTTGA
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT

P_AA02949 1633 TCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT

P_AA02949 1693 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT
DNA35639 1741 TAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAATG

P_AA02949 1753 TAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAATG
DNA35639 1801 TTTGTATGA

P_AA02949 1813 TTTGTATGA

>14 P_AA65278 Human secreted protein gene 29. (1932 bp) [1 seg]
Score = 1785 (3539 bits), Expect = 0.0
Identities = 1804/1810 (99%), Gaps = 2/1810 (0%), at 4,9-1813,1816, Strand +/-

DNA35639 4 GCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG

P_AA65278 9 GCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-SCTCGG
DNA35639 64 CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGG

P_AA65278 68 CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGG
DNA35639 124 CCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGC

P_AA65278 128 CCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGC

BLAST RESULTS A-30

DNA35639	184	TGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGT

P_AA65278	188	TGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGT
DNA35639	244	TGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGG

P_AA65278	248	TGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACANCTTGACGGGGAGG
DNA35639	304	TGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAA

P_AA65278	308	TGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAA
DNA35639	364	AGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCT

P_AA65278	368	AGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCT
DNA35639	424	TGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAG

P_AA65278	428	TGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAG
DNA35639	484	ACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCC

P_AA65278	488	ACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCC
DNA35639	544	ACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTC

P_AA65278	548	ACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTC
DNA35639	604	TCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTA

P_AA65278	608	TCCAGGGTGTGCCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTA
DNA35639	664	AGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCAC

P_AA65278	668	AGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCAC
DNA35639	724	CAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTG

P_AA65278	728	CAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTG
DNA35639	784	GAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGG

P_AA65278	788	GAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTG-CCAATGTAATGTGACGCTGG
DNA35639	844	AAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTG

P_AA65278	847	AAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTG
DNA35639	904	GACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGG

P_AA65278	907	GACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGG
DNA35639	964	AGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCAAGA

P_AA65278	967	AGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCAAGA

BLAST RESULTS A-31

DNA35639	1024	GCTCAGACACAATCTCCAAGAATGGGACCCCTTTCTCTGTACCTCCGCACGAGCCCTCC

P_AA265278	1027	GCTCAGACACAATCTCCAAGAATGGGACCCCTTTCTCTGTACCTCCGCACGAGCCCTCC
DNA35639	1084	GGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCC

P_AA265278	1087	GGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCC
DNA35639	1144	AGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCC

P_AA265278	1147	AGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCC
DNA35639	1204	CCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGG

P_AA265278	1207	CCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGG
DNA35639	1264	TGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAG

P_AA265278	1267	TGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAG
DNA35639	1324	GATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGA

P_AA265278	1327	GATTTGGGGTCTCTCCTTCCTATARGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGA
DNA35639	1384	AAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACC

P_AA265278	1387	AAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACC
DNA35639	1444	ATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATT

P_AA265278	1447	ATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATT
DNA35639	1504	GGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTA

P_AA265278	1507	GGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTA
DNA35639	1564	CTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCT

P_AA265278	1567	CTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCT
DNA35639	1624	GTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATA

P_AA265278	1627	GTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATA
DNA35639	1684	ACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAA

P_AA265278	1687	ACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAA
DNA35639	1744	AACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTT

P_AA265278	1747	AACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTT
DNA35639	1804	GTATGAAAAA

P_AA265278	1807	GTATGARAAA

BLAST RESULTS A-32

>15 P_AAF45017 Human secreted protein related coding sequence SEQ ID NO: 141.
 (1869_bp) [1 seg]
 Score = 1731 (3431 bits), Expect = 0.0
 Identities = 1795/1812 (99%), Gaps = 4/1812 (0%), at 1,28-1809,1838, Strand +/+

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

P_AAF45017	28	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

P_AAF45017	88	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639	121	GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

P_AAF45017	148	GGGCCATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGNTGCGGTTTTTGTTCCTGG
DNA35639	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC

P_AAF45017	208	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639	241	GGTTGCAGGCGGTGGAGG-GAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGG
		***** * * * *
P_AAF45017	268	GGTTGCAGGCGGTGGAGGAGGGGAAAGTGGTGCTT-CAGCATGGTACACCTGCACAGG
DNA35639	300	GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA

P_AAF45017	327	GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA
DNA35639	360	GAAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA

P_AAF45017	387	GAAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA
DNA35639	420	TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGGTGGAGGGTCTCCAGGAG

P_AAF45017	447	TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGGTGGAGGGTCTCCAGGAG
DNA35639	480	AAAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG

P_AAF45017	507	AAAGACTCTGGCCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG
DNA35639	540	GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC

P_AAF45017	567	GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC
DNA35639	600	CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG

P_AAF45017	627	CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG
DNA35639	660	AGTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT

P_AAF45017	687	AGTAAGCCCGTTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT
DNA35639	720	GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATG

P_AAF45017	747	GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATG

BLAST RESULTS A-33

DNA35639 780 GCTGGAGTCTATGTCTGCAAGGCCCAACAATGAGGTGGGCACTGCCCAATGTAATGTGACG

P_AAF45017 807 GCTGGAGTCTATGTCTGCAAGGCCCAACAATGAGGTGGGCACTGCCCAATGTAATGTGACG

DNA35639 840 CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTG

P_AAF45017 867 CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGAAGCTGTTGTGGGTACCCTG

DNA35639 900 GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTG

P_AAF45017 927 GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTG

DNA35639 960 GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCC

P_AAF45017 987 GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCC

DNA35639 1020 AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTGCACCTCCGCACGAGCC

P_AAF45017 1047 AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCTCTGTGCACCTCCGCACGAGCC

DNA35639 1080 CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCC

P_AAF45017 1107 CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTATCC

DNA35639 1140 AGCCAGGCCCTGCCCTCACCAAGAC-TGCCCACGACAGATGGGGCCACCCCTCAACCAAT

P_AAF45017 1167 AGCCAGGCCCTGCCCTCACCAAGACATGCCCACGACAGATGGGGCCACCCCTCAACCAAT

DNA35639 1199 ATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGC-TTGAGCCGCATGGGTGCTGTGCCTG

P_AAF45017 1227 ATCCCCCATCCCTGGTGGGGTTTTTCTTTGGCTTTGAGCCGCATGGGTGCTGNGCCTG

DNA35639 1258 TGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGG

P_AAF45017 1287 TGATGGNGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGG

DNA35639 1318 CTAAAGGATTTGGGGTCTCTCTCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTC

P_AAF45017 1347 CTAAAGGATTTGGGGTCTCTCTCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTC

DNA35639 1378 ATGGGAAGAGTCACTCTCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGG

P_AAF45017 1407 ATGGGAAGAGTCACTCTCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGG

DNA35639 1438 AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT

P_AAF45017 1467 AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT

DNA35639 1498 GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT

P_AAF45017 1527 GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT

DNA35639 1558 TAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCT

P_AAF45017 1587 TAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCT

DNA35639 1618 TGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCCTCCAGCTCCCTGTATT

BLAST RESULTS A-34

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P_AAF45017 1647 TGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATT
DNA35639 1678 GATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCT
*****
P_AAF45017 1707 GATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCT
DNA35639 1738 TATTAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATA
*****
P_AAF45017 1767 TATTAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATA
DNA35639 1798 ATGTTTGTATGA
*****
P_AAF45017 1827 ATGTTTGTATGA

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>16 P_AAF45016 Human secreted protein related coding sequence SEQ ID NO: 139.
(1869 bp) [1 seg]
Score = 1731 (3431 bits), Expect = 0.0
Identities = 1795/1812 (99%), Gaps = 4/1812 (0%), at 1,28-1809,1838, Strand +/+

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DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
*****
P_AAF45016 28 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
*****
P_AAF45016 88 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG
*****
P_AAF45016 148 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGNTGCGGTTTTTGTTCCTGG
DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC
*****
P_AAF45016 208 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC
DNA35639 241 GGTTCAGGCGGTGGAGG-GAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGG
*****
P_AAF45016 268 GGTTCAGGCGGTGGAGGAGGGGAAAGTGGTGCTT-CAGCATGGTACACCTTGCACAGG
DNA35639 300 GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA
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P_AAF45016 327 GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA
DNA35639 360 GAAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA
*****
P_AAF45016 387 GAAAAGGAGGATCAGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA
DNA35639 420 TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAG
*****
P_AAF45016 447 TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGGTGGAGGGTCTCCAGGAG
DNA35639 480 AAAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG
*****
P_AAF45016 507 AAAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG
DNA35639 540 GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGC

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BLAST RESULTS A-35

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*****
P_AAF45016 567 GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC
DNA35639 600 CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG
*** *****
P_AAF45016 627 CGTATCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG
DNA35639 660 AGTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT
*****
P_AAF45016 687 AGTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT
DNA35639 720 GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATG
*****
P_AAF45016 747 GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATG
DNA35639 780 GCTGGAGTCTATGTCTGCAAGGCCCAACAATGAGGTGGGCACTGCCCAATGTAATGTGACG
*****
P_AAF45016 807 GCTGGAGTCTATGTCTGCAAGGCCCAACAATGAGGTGGGCACTGCCCAATGTAATGTGACG
DNA35639 840 CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTG
*****
P_AAF45016 867 CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGAAGCTGTTGTGGGTACCCTG
DNA35639 900 GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTG
*****
P_AAF45016 927 GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTG
DNA35639 960 GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC
*****
P_AAF45016 987 GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC
DNA35639 1020 AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCC
*****
P_AAF45016 1047 AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCC
DNA35639 1080 CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCC
*****
P_AAF45016 1107 CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTATCC
DNA35639 1140 AGCCAGGCCCTGCCCTCACCAAGAC-TGCCACGACAGATGGGGCCACCCCAACCAAT
*****
P_AAF45016 1167 AGCCAGGCCCTGCCCTCACCAAGACATGCCACGACAGATGGGGCCACCCCAACCAAT
DNA35639 1199 ATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGC-TTGAGCCGCATGGGTGCTGTGCCTG
*****
P_AAF45016 1227 ATCCCCCATCCCTGGTGGGGTTTCTTCCTTTGGCTTTGAGCCGCATGGGTGCTGNGCCTG
DNA35639 1258 TGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTTGG
*****
P_AAF45016 1287 TGATGGNGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTTGG
DNA35639 1318 CTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTC
*****
P_AAF45016 1347 CTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTC
DNA35639 1378 ATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGG
*****

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BLAST RESULTS A-36

P_AAF45016 1407 ATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGG
 DNA35639 1438 AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT

 P_AAF45016 1467 AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT
 DNA35639 1498 GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT

 P_AAF45016 1527 GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT
 DNA35639 1558 TAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCT

 P_AAF45016 1587 TAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCT
 DNA35639 1618 TGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATT

 P_AAF45016 1647 TGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATT
 DNA35639 1678 GATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCT

 P_AAF45016 1707 GATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCT
 DNA35639 1738 TATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATA

 P_AAF45016 1767 TATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATA
 DNA35639 1798 ATGTTTGTATGA

 P_AAF45016 1827 ATGTTTGTATGA

>17 P_AAF45014 Human secreted protein related coding sequence SEQ ID NO: 135.
 (1869 bp) [1 seg]
 Score = 1731 (3431 bits), Expect = 0.0
 Identities = 1795/1812 (99%), Gaps = 4/1812 (0%), at 1,28-1809,1838, Strand +/+

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT

 P_AAF45014 28 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
 DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA

 P_AAF45014 88 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA
 DNA35639 121 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG

 P_AAF45014 148 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGNTGCGGTTTTTGTTCCTGG
 DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC

 P_AAF45014 208 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC
 DNA35639 241 GGTTGCAGGCGGTGGAGG-GAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGG

 P_AAF45014 268 GGTTGCAGGCGGTGGAGGAGGGGAAAGTGGTGCTT-CAGCATGGTACACCTTGACAGG
 DNA35639 300 GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA

BLAST RESULTS A-37

P_AAF45014 327 GAGGCGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAA
DNA35639 360 GAAAAGGAGGATCAGGTGTTGTCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA

P_AAF45014 387 GAAAAGGAGGATCAGGTGTTGTCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTA
DNA35639 420 TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGGCTGGAGGGTCTCCAGGAG

P_AAF45014 447 TCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGGTGGAGGGTCTCCAGGAG
DNA35639 480 AAAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG

P_AAF45014 507 AAAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG
DNA35639 540 GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC

P_AAF45014 567 GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGC
DNA35639 600 CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG

P_AAF45014 627 CGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG
DNA35639 660 AGTAAGCCCGCTGTCCAATACCACTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT

P_AAF45014 687 AGTAAGCCCGCTGTCCAATACCACTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTT
DNA35639 720 GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATG

P_AAF45014 747 GCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATG
DNA35639 780 GCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACG

P_AAF45014 807 GCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCACTGCCCAATGTAATGTGACG
DNA35639 840 CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTG

P_AAF45014 867 CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGAAGCTGTTGTGGGTACCCTG
DNA35639 900 GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTTGTACCACCGCCGGGGCAAGGCCCTG

P_AAF45014 927 GTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTTGTACCACCGCCGGGGCAAGGCCCTG
DNA35639 960 GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC

P_AAF45014 987 GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC
DNA35639 1020 AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCC

P_AAF45014 1047 AAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCGCACGAGCC
DNA35639 1080 CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCC

P_AAF45014 1107 CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTATCC
DNA35639 1140 AGCCAGGCCCTGCCCTCACCAAGAC-TGCCACGACAGATGGGGCCACCCTCAACCAAT

P_AAF45014 1167 AGCCAGGCCCTGCCCTCACCAAGACATGCCACGACAGATGGGGCCACCCTCAACCAAT

BLAST RESULTS A-28

DNA35639	1199	ATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGC-TTGAGCCGCATGGGTGCTGTGCCTG *****
P_AAF45014	1227	ATCCCCCATCCCTGGTGGGGTTTTTCTCTTGGCTTTGAGCCGCATGGGTGCTGNGCCTG
DNA35639	1258	TGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGG *****
P_AAF45014	1287	TGATGGNGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACTCATTGG
DNA35639	1318	CTAAAGGATTTGGGGTCTCTCCTTCCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTC *****
P_AAF45014	1347	CTAAAGGATTTGGGGTCTCTCCTTCCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTC
DNA35639	1378	ATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGG *****
P_AAF45014	1407	ATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGG
DNA35639	1438	AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT *****
P_AAF45014	1467	AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT
DNA35639	1498	GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT *****
P_AAF45014	1527	GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT
DNA35639	1558	TAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCT *****
P_AAF45014	1587	TAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCT
DNA35639	1618	TGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATT *****
P_AAF45014	1647	TGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATT
DNA35639	1678	GATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCT *****
P_AAF45014	1707	GATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCT
DNA35639	1738	TATTAATACTAATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATA *****
P_AAF45014	1767	TATTAATACTAATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATA
DNA35639	1798	ATGTTTGTATGA *****
P_AAF45014	1827	ATGTTTGTATGA

BLAST RESULTS A-39